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ID   AX004614     standard; DNA; PRO; 327 BP.
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SV   AX004614.1
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DT   24-AUG-2000 (Rel. 64, Created)
DT   24-AUG-2000 (Rel. 64, Last updated, Version 1)
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DE   Sequence 2 from Patent WO9915669.
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KW   .
XX
OS   Clostridium perfringens
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC   Clostridiales; Clostridiaceae; Clostridium.
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RN   [1]
RA   Gibert M., Popoff M.R.;
RT   "Clostridium toxin, and method for preparing immunogenic compositions";
RL   Patent number WO9915669-A/2, 01-APR-1999.
RL   GIBERT MARYSE (FR);
RL   PASTEUR INSTITUT (FR).
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FH   Key             Location/Qualifiers
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FT                   /db_xref="taxon:1502"
FT                   /organism="Clostridium perfringens"
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     aaagtgttct cggggggacac ttttttgttt taaaaaggaa aatataaata aaatttagat      180
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AC   AP003515;
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SV   AP003515.1
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DT   02-AUG-2001 (Rel. 68, Created)
DT   22-JAN-2002 (Rel. 70, Last updated, Version 3)
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DE   Clostridium perfringens plasmid pCP13 DNA, complete sequence.
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OS   Clostridium perfringens
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC   Clostridiales; Clostridiaceae; Clostridium.
OG   Plasmid pCP13
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RN   [1]
RP   1-54310
RA   Shimizu T.;
RT   ;
RL   Submitted (12-APR-2001) to the EMBL/GenBank/DDBJ databases.
RL   Tohru Shimizu, Institute of Basic Medical Sciences, University of Tukuba,
RL   Department of Microbiology; 1-1-1 Tennohdai, Tsukuba, Ibaraki 305-8575,
RL   Japan (E-mail:tshimizu@md.tsukuba.ac.jp, Tel:81-298-53-3354,
RL   Fax:81-298-53-3354)
XX
RN   [2]
RA   Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T.,
RA   Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT   "Complete genome sequence of Clostridium perfringens, an anaerobic
RT   flesh-eater";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
XX
DR   SPTREMBL; Q93M84; Q93M84.
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DR   SPTREMBL; Q93M90; Q93M90.
DR   SPTREMBL; Q93M91; Q93M91.
DR   SPTREMBL; Q93M92; Q93M92.
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DR   SPTREMBL; Q93MA1; Q93MA1.
DR   SPTREMBL; Q93MA2; Q93MA2.
DR   SPTREMBL; Q93MA3; Q93MA3.
DR   SPTREMBL; Q93MA4; Q93MA4.
DR   SPTREMBL; Q93MA5; Q93MA5.
DR   SPTREMBL; Q93MA6; Q93MA6.
DR   SPTREMBL; Q93MA7; Q93MA7.
DR   SPTREMBL; Q93MA8; Q93MA8.
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DR   SPTREMBL; Q93MB1; Q93MB1.
DR   SPTREMBL; Q93MB2; Q93MB2.
DR   SPTREMBL; Q93MB3; Q93MB3.
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DR      SPTREMBL;  Q93ME4;  Q93ME4.
DR      SPTREMBL;  Q93ME5;  Q93ME5.
DR      SPTREMBL;  Q93ME6;  Q93ME6.
DR      SWISS-PROT;  Q93MD2;  RES1_CLOPE.
DR      SWISS-PROT;  Q93MD5;  YU12_CLOPE.
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FT                      inhibitor soj from Bacillus subtilis (253 aa); 37% identity
FT                      in 250 aa overlap"
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FT                      DSIEEIKDEFNPNLNFKGCFITMDSSTTVNKVIKQELKSVLGEKMFNTSIHQNIKVVES
FT                      TFEECPVVFSSKKARASLNYKDLSKEIF"
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FT                      protein from Lactococcus lactis subsplactis (242 aa); 30%
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FT                           aa overlap"
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FT                           overlap"
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FT                                AIKHTIKNTKKIEEEIIRCLKFVGLEGCQKNYIYELSGGEQQRVAIARLMLKPSEIILA
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FT                                overlap"
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FT                                VQIENEQILDKLIEDLKSESIIVQKRVMGDSSQYNTETLKIILVVCFIGLIFMIFYQVL
FT                                GSYKKIGIQKLLGHSTFVMLKERLLEVLRIEVIVMLVVTVLLVFFNFKTFNSLFWKFML
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FT                                INGLEKYYDMSVYLIDPYNLYDNVASTIINIKAKVKVIIFAIVILLAVISIIILQNTSL
FT                                YFNQNKNKIIVKKLHGYRLIYRYMNYFIMVLITWTCPLAIASLITKDINIIYFTLILVV
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FT                                /note="77 aa, similar to probable transposase from Yersinia
FT                                pestis plasmid pMT1 (402 aa); 25% identity in 158 aa
FT                                overlap"
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FT                              pIP404 (166 aa); 25% identity in 156 aa overlap"
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FT                              product from Bacillus halodurans (211 aa); 25% identity in
FT                              196 aa overlap"
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FT                          Clostridium perfringens (265 aa); 91% identity in 265 aa
FT                          overlap"
FT                          /note="PCP17"
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FT                          /product="beta2-toxin"
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FT                          39% identity in 101 aa overlap"
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FT                           /note="145 aa, similar to prf:2605291A RadC protein from
FT                           Bacillus sp. (119 aa); 54% identity in 119 aa overlap"
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FT        CDS                16820..17137
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FT                           /db_xref="SPTREMBL:Q93MC5"
FT                           /note="105 aa, partially similar to gp:AF225463_1 SpoIIGB
FT                           from Clostridium bifermentans (107 aa); 34% identity in 73
FT                           aa overlap"
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FT                           IENNINLNREIIEVLIYAKEYKTIVNIKKIFVLGLKGNEMIINKNDDLYRCIEEKVYLG
FT                           N"
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FT                           EEKEDQNLLIIEGKYKGENPKLKYCFNGIYEMNKYLINIRSKYETLTKTLLIKVNLIVR
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FT                           GYFRKLDKNELKNITELVNENN"
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FT                           DESLKGTLEIFKYSDDEISSISLNDLIVECKDLLENWLRENKSINENFNIIPYEILNSS
FT                           MDKLLELVEDSIFFDEAFKNMIEKE"
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FT                         FNALIENRFGDSQEKRELTDFKSMNSLKVFFDKVYETEVTRAIEKSDYSFEFNLDLGRK
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FT                         slr1999 from Synechocystis sp. (strain PCC 6803) (136 aa);
FT                         45% identity in 53 aa overlap"
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FT                         KDLPIGTVRSIFKQAGIKIL"
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FT                         /note="138 aa, similar to pir:T13557 hypothetical protein
FT                         17 from Bacillus phage phi-105 (138 aa); 48% identity in
FT                         134 aa overlap"
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FT                         /note="252 aa, no significant homology"
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FT                         EEKYNLAKEYVENKRQLYGYNSSKVLYFPYERQTAGNWCGPAAAYNAIIGANPSYKGKI
FT                         SQNSLAMTLKTGVPGDKGTDFPGEWKRTMNNYLGANNYEISKGSSYSYSDWRNRVKNSV
FT                         IWTVDKGYAVIADTKQSPYGTKLHPNYNYIDDRGPGGKPTYHYIAITGYDDTPGNDRML
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FT                         product from Bacillus halodurans (338 aa); 23% identity in
FT                         343 aa overlap"
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FT                         IDTGNISEINNMTPSYIPTISIDNDYLVYSRLNESNFELVLLNLMDKDLVILETLNSES
FT                         NEKISIPSISENLIVWSKSNGNYSNLSSNIYMYDISKDSKILLSENNSIIKPQIKNNII
FT                         IATNIKDNSDFTESYLTKYDLKNSKWNEFISNKSKVYNDVKNLSVDDPLIGENYISWWD
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FT                          KILSTPGEHSWFNLKEGGNSYLVSKSSYESKEPIYVKKCDKIYIKFSSIPKEVTVKEIS
FT                          NSPYITYEHFESNSKKEYFFFSPDQIGKYIFEVRGSWDDTHTISEIFSVYVN"
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FT                          /note="61 aa, similar to gp:AF179847_5 putative resolvase
FT                          from Lactococcus lactis (199 aa); 38% identity in 65 aa
FT                          overlap"
FT                          /note="truncated"
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FT                          RLGENRKETKELKLFL"
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FT                          SVSKLESELKSVNSTESKGSELNDSTKDKKAEDKIKDESSNKILENVKNRYIQFGKDEG
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FT                          IE"
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FT                          /note="453 aa, partially similar to sp:PRIM_CLOAB DNA
FT                          PRIMASE (EC 2.7.7.-) from Clostridium acetobutyricum (596
FT                          aa); 21% identity in 402 aa overlap"
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FT                          KVIPLHFDIGDGYVNDLKELINKELKSARYEDLRNSIDNTLDNKEKAFKKEVEPFYDIN
FT                          KLKEIPIGDIADKLGIDTVKRGNKLWCNLRGEKTASCCINIDKNYFYDFGGQPEGGDGI
FT                          KFVSKAEGISAKDSIYRLADMFGIEPENNIDNSFKPSFHISNSDYKEIGIEPNRAMLNV
FT                          DINLERQSLAEVMELEKSCAKTMNELANDDKSTFLNILNFKSMPIVYNNAKTYYSCIER
FT                          INEYVKEYNSPIDGFNSLEVLLYKDFTKSLEEKLNKQIDILYRAGINERIGFDLSEEKV
FT                          NLKKDLDDLFSASLSNGVEVYYNSNPDELKVIKSIEEFRDYAIDILVPELSGFEVSEEE
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FT                          Bacillus anthracis (589 aa); 28% identity in 500 aa
FT                          overlap"
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FT                              KDKEKLLKEVKETTKEFIETIESSLLNIKEKEILIEDEAVKEFLGKDKVKINELSKKEL
FT                              EELIEKNNSYTWFKIDENKEIDSKNFTGKNHVMVVKEDDSYRDIYVGKTYNLENLIYVD
FT                              DNKNLYRLKKELEVEKTNNSFFYKKNESEVLSMEYEKDINLSSDKFISDENRELNEKGV
FT                              FKEPYITVDFCEENFFKKGEVIDLKEAK"
FT       CDS                    complement(27506..27670)
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FT                              IINANIEVK"
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FT                              /note="72 aa, no significant homology"
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FT                              QKEEDNTMILAVDINNKSIIEDYNYEV"
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FT                              /note="377 aa, similar to gp:AF188935_83 pXO2-84 from
FT                              Bacillus anthracis (490 aa); 31% identity in 421 aa
FT                              overlap"
FT                              /note="plasmid-related"
FT                              /transl_table=11
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FT                              SENGALDEEKIQEATRRAMEELSKREGFKDLTWSASLHYNTDNIHVHIASVEINPSRER
FT                              GKFKPRTLYNMKSSFVNSLLDKQKDLDKINLLIRDNLIQGKKEMSFKEDIEMRKMVKEI
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FT                              Bacillus anthracis (282 aa); 25% identity in 227 aa
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FT                              protein homolog yvcE from Bacillus subtilis (473 aa); 47%
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FT                   overlap"
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FT                   FNAQIFNVLSMLWNNALTQGLPEKKAFDEGKKTVEESKKYLLLLDESHRIINSNNILAV
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FT                   /db_xref="SPTREMBL:Q93MA0"
FT                   /note="703 aa, similar to gp:AF007787_9 type I
FT                   topoisomerase from Enterococcus faecalis (714 aa); 31%
FT                   identity in 742 aa overlap"
FT                   /note="PCP47"
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FT                   /product="type I topoisomease"
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FT                   SKLFSLSKLQSLLSKKYKMTFKESLELIQKLYEKGFVTYPRTNTEYLAEAEKGKVKEII
FT                   DILCSEGYNLEFKDKKTIFDDSKIESHSAITPTVKIPKEDELKGKMLDVYNTIKNRFIS
FT                   NFLIEETLIDRTIIRIEVGDLEFSLKGDVIVQKGFLEYEPIKKDENTLPNLNVGDKINT
FT                   NFKAIEKVTQAPGKMTTEMLSNYLKNPFKNYEIENEEEDYKAILDGLEIGTEATRTGII
FT                   ENAKKYKYISENKSVLSIEPLGRKLIETLDKLNVNLSKEKTVEFSRILKKVYKNELNID
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FT                   /note="214 aa, similar to gp:AF188935_10 pXO2-10 from
FT                   Bacillus anthracis (222 aa); 23% identity in 222 aa
FT                   overlap"
FT                   /note="plasmid-related"
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FT                   /gene="PCP48"
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